



PCT

RAW SEQUENCE LISTING

DATE: 07/12/2005

PATENT APPLICATION: US/10/509,950

TIME: 10:21:28

Input Set : A:\US10509950 Sequence Listing.txt

Output Set: N:\CRF4\07122005\J509950.raw

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3 <110> APPLICANT: Evotec NeuroSciences GmbH
5 <120> TITLE OF INVENTION: cAMP-Regulated Phosphorprotein for Diagnostic and
6   Therapeutic Use in Neurodegenerative Diseases
8 <130> FILE REFERENCE: 020880ep
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/509,950
C--> 11 <141> CURRENT FILING DATE: 2004-10-04
13 <160> NUMBER OF SEQ ID NOS: 16
15 <170> SOFTWARE: PatentIn Ver. 2.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 813
19 <212> TYPE: PRT
20 <213> ORGANISM: Homo sapiens
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27           20           25           30
29 Ser Leu Asp Glu Glu Glu Lys Leu Glu Leu Gln Arg Arg Leu Glu Ala
30           35           40           45
32 Gln Asn Gln Glu Arg Arg Lys Ser Lys Ser Gly Ala Gly Lys Gly Lys
33           50           55           60
35 Leu Thr Arg Ser Leu Ala Val Cys Glu Glu Ser Ala Arg Pro Gly
36   65           70           75           80
38 Gly Glu Ser Leu Gln Asp Gln Glu Ser Ile His Leu Gln Leu Ser Ser
39           85           90           95
41 Phe Ser Ser Leu Gln Glu Glu Asp Lys Ser Arg Lys Asp Asp Ser Glu
42           100          105          110
44 Arg Glu Lys Glu Lys Asp Lys Asn Lys Asp Lys Thr Ser Glu Lys Pro
45           115          120          125
47 Lys Ile Arg Met Leu Ser Lys Asp Cys Ser Gln Glu Tyr Thr Asp Ser
48           130          135          140
50 Thr Gly Ile Asp Leu His Glu Phe Leu Ile Asn Thr Leu Lys Asn Asn
51   145          150          155          160
53 Ser Arg Asp Arg Met Ile Leu Leu Lys Met Glu Gln Glu Ile Ile Asp
54           165          170          175
56 Phe Ile Ala Asp Asn Asn Asn His Tyr Lys Lys Phe Pro Gln Met Ser
57           180          185          190
59 Ser Tyr Gln Arg Met Leu Val His Arg Val Ala Ala Tyr Phe Gly Leu
60           195          200          205
62 Asp His Asn Val Asp Gln Thr Gly Lys Ser Val Ile Ile Asn Lys Thr
63           210          215          220
65 Ser Ser Thr Arg Ile Pro Glu Gln Arg Phe Cys Glu His Leu Lys Asp
66   225          230          235          240

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68 Glu Lys Gly Glu Glu Ser Gln Lys Arg Phe Ile Leu Lys Arg Asp Asn
69                245                250                255
71 Ser Ser Ile Asp Lys Glu Asp Asn Gln Ser Val Cys Ser Gln Glu Ser
72                260                265                270
74 Leu Phe Val Glu Asn Ser Arg Leu Leu Glu Asp Ser Asn Ile Cys Asn
75                275                280                285
77 Glu Thr Tyr Lys Lys Arg Gln Leu Phe Arg Gly Asn Arg Asp Gly Ser
78                290                295                300
80 Gly Arg Thr Ser Gly Ser Arg Gln Ser Ser Ser Glu Asn Glu Leu Lys
81 305                310                315                320
83 Trp Ser Asp His Gln Arg Ala Trp Ser Ser Thr Asp Ser Asp Ser Ser
84                325                330                335
86 Asn Arg Asn Leu Lys Pro Ala Met Thr Lys Thr Ala Ser Phe Gly Gly
87                340                345                350
89 Ile Thr Val Leu Thr Arg Gly Asp Ser Thr Ser Ser Thr Arg Ser Thr
90                355                360                365
92 Gly Lys Leu Ser Lys Ala Gly Ser Glu Ser Ser Ser Ser Ala Gly Ser
93                370                375                380
95 Ser Gly Ser Leu Ser Arg Thr His Pro Pro Leu Gln Ser Thr Pro Leu
96 385                390                395                400
98 Val Ser Gly Val Ala Ala Gly Ser Pro Gly Cys Val Pro Tyr Pro Glu
99                405                410                415
101 Asn Gly Ile Gly Gly Gln Val Ala Pro Ser Ser Thr Ser Tyr Ile Leu
102                420                425                430
104 Leu Pro Leu Glu Ala Ala Thr Gly Ile Pro Pro Gly Ser Ile Leu Leu
105                435                440                445
107 Asn Pro His Thr Gly Gln Pro Phe Val Asn Pro Asp Gly Thr Pro Ala
108                450                455                460
110 Ile Tyr Asn Pro Pro Thr Ser Gln Gln Pro Leu Arg Ser Ala Met Val
111 465                470                475                480
113 Gly Gln Ser Gln Gln Gln Pro Pro Gln Gln Gln Pro Ser Pro Gln Pro
114                485                490                495
116 Gln Gln Gln Val Gln Pro Pro Gln Pro Gln Met Ala Gly Pro Leu Val
117                500                505                510
119 Thr Gln Ser Val Gln Gly Leu Gln Ala Ser Ser Gln Ser Val Gln Tyr
120                515                520                525
122 Pro Ala Val Ser Phe Pro Pro Gln His Leu Leu Pro Val Ser Pro Thr
123                530                535                540
125 Gln His Phe Pro Met Arg Asp Asp Val Ala Thr Gln Phe Gly Gln Met
126 545                550                555                560
128 Thr Leu Ser Arg Gln Ser Ser Gly Glu Thr Pro Glu Pro Pro Ser Gly
129                565                570                575
131 Pro Val Tyr Pro Ser Ser Leu Met Pro Gln Pro Ala Gln Gln Pro Ser
132                580                585                590
134 Tyr Val Ile Ala Ser Thr Gly Gln Gln Leu Pro Thr Gly Gly Phe Ser
135                595                600                605
137 Gly Ser Gly Pro Pro Ile Ser Gln Gln Val Leu Gln Pro Pro Pro Ser
138                610                615                620
140 Pro Gln Gly Phe Val Gln Gln Pro Pro Pro Ala Gln Met Pro Val Tyr

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141 625                630                635                640
143 Tyr Tyr Pro Ser Gly Gln Tyr Pro Thr Ser Thr Thr Gln Gln Tyr Arg
144                645                650                655
146 Pro Met Ala Pro Val Gln Tyr Asn Ala Gln Arg Ser Gln Gln Met Pro
147                660                665                670
149 Gln Ala Ala Gln Gln Ala Gly Tyr Gln Pro Val Leu Ser Gly Gln Gln
150                675                680                685
152 Gly Phe Gln Gly Leu Ile Gly Val Gln Gln Pro Pro Gln Ser Gln Asn
153                690                695                700
155 Val Ile Asn Asn Gln Gln Gly Thr Pro Val Gln Ser Val Met Val Ser
156 705                710                715                720
158 Tyr Pro Thr Met Ser Ser Tyr Gln Val Pro Met Thr Gln Gly Ser Gln
159                725                730                735
161 Gly Leu Pro Gln Gln Ser Tyr Gln Gln Pro Ile Met Leu Pro Asn Gln
162                740                745                750
164 Ala Gly Gln Gly Ser Leu Pro Ala Thr Gly Met Pro Val Tyr Cys Asn
165                755                760                765
167 Val Thr Pro Pro Thr Pro Gln Asn Asn Leu Arg Leu Ile Gly Pro His
168                770                775                780
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171 785                790                795                800
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174                805                810
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186 gaactgcaga ggcggctgga ggctcagaat caagaaaagaa gaaaatccaa gtcaggagca 180
187 ggaaaaggta aactgactcg cagyccttgc gtctgtgagg aatcttctgc cagaccagga 240
188 ggtgaaagtc ttcaggatca ggaatcaatt catttacagc tttccagttt ttccagcctg 300
189 caagaggagc ataaatctag gaaatcagac tctgaaagag aaaaagaaaa ggataaaaaac 360
190 aaagataaaaa cctctgaaaa acccaagatc agaatgttat caaaagattg cagccaagaa 420
191 tacacggatt ctacaggcat agacttacac gagtttctga ttaacacatt aaagaataat 480
192 tccaggggaca ggatgatact tttgaaaatg gagcaggaaa ttattgattt cattgctgac 540
193 aacaataatc attataaaaa gttccctcag atgtcatcgt atcagaggat gcttgtccat 600
194 cgagtggcag cttatttttg attggatcac aatgtggatc aaacaggaaa atctgttatc 660
195 atcaacaaga ccagcagcac cagaatacca gagcaaaggt tttgtgaaca tttaaaagat 720
196 gaaaaagggtg aagaatccca gaagcggttt atcttgaagc gagataactc tagtattgat 780
197 aaagaagaca atcagtcagt ttgctcccag gaaagccttt ttgtggaaaa cagtaggctc 840
198 ttggaagaca gtaacatatg caatgagacc tataagaaaa gacagctctt tcggggcaac 900
199 agagatggct caggggagaac atctgggagt cgacagagca gctcagaaaa tgaactcaag 960
200 tggctctgacc accaaaagggc ctggagcagc acagactccg acagttccaa ccgcaatcta 1020
201 aagcccgccca tgaccaagac ggcgagtttt gggggcatca cgggtctgac caggggtgac 1080
202 agcacttcca gtactaggag taccgggaag ctgtccaaaag caggttccga gtcttcacgc 1140
203 agtgcaggct cctcaggatc gctgtcccgc acccatccac ctctccagag cacaccctta 1200
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205 ggccaggttg ctcccagcag caccagctac atcctccttc cacttgaagc tgcaaacaggc 1320
206 atcccgcttg gaagcatcct tcttaatcca cacacaggcc agccctttgt gaatcccgat 1380
207 ggaactcctg caatatacaa cccacccacc agtcagcagc ccctgcgaag cgccatggtg 1440
208 gggcagtcct aacagcagcc gccacagcag cagccctccc cgcagcccca acagcaggtc 1500
209 cagccaccgc agccacagat ggcaggccct ctggtcactc agtctgtcca ggggctgcag 1560
210 gcttcctccc agtcagtgc atatacggca gtctcttttc ctcccagca cctcctacct 1620
211 gtgtctccaa cgcagcactt tcccagaga gatgatgtgg caacacagtt tggccagatg 1680
212 accctgagcc ggcagtcctc gggggagact cctgaacccc catcagggtc tgtctaccca 1740
213 tcctccctta tgccacagcc ggcccagcag cccagctatg taatcgctc tacaggccag 1800
214 cagcttccta caggaggatt ctcaggctct ggccctccca tctcccagca ggtcctccag 1860
215 cccctccct caccacaggg atcgtgcaa cagcctccgc ctgcacagat gcctgtatat 1920
216 tattacccat ctggtcagta ccctacctca accacgcaac agtaccggcc catggccccc 1980
217 gttcagtaca acgctcagag gagtcaacag atgccacagg cagcacagca agcaggttac 2040
218 cagccagtct tgtctggtca acagggattc caaggcctaa taggagtgc gcagccacct 2100
219 cagagtcaga acgtgataaa taaccaacaa ggaactccgg tgcaaaagct gatggtttcc 2160
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223 attggccac actgcccctc cagcactgtc ccagtgtgt cagctagctg cagaacaaac 2400
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238 cggccactcc agagaacggc attgttaa atcagaaagtct ggatgaagag gagaaactgg 360
239 aactgcagag gcggctggag gctcagaatc aagaaagaag aaaatccaag tcaggagcag 420
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241 gtgaaagtct tcaggatcag gaatcaattc atttacagct ttccagtttt tccagcctgc 540
242 aagaggagga taaatctagg aaagatgact ctgaaagaga aaaagaaaag gataaaaaaca 600
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244 acacggattc tacaggcata gacttacacg agtttctgat taacacatta aagaataatt 720
245 ccaggggacag gatgatactt ttgaaaatgg agcaggaaat tattgatttc attgctgaca 780
246 acaataatca ttataaaaag ttccctcaga tgtcatcgta tcagaggatg cttgtccatc 840
247 gagtggcagc ttattttgga ttggatcaca atgtggatca aacaggaaaa tctgttatca 900
248 tcaacaagac cagcagcacc agaataccag agcaaagggt ttgtgaacat ttaaaagatg 960
249 aaaaagggtga agaatcccag aagcggttta tcttgaagcg agataaactct agtattgata 1020
250 aagaagacaa tcagtcagtt tgctcccagg aaagcctttt tgtggaaaac agtaggctct 1080
251 tggaaagacag taacatatgc aatgagacct ataagaaaag acagctcttt cggggcaaca 1140
252 gagatggctc agggagaaca tctgggagtc gacagagcag ctcaaaaaat gaactcaagt 1200
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254 agcccgccat gaccaagacg gcgagttttg ggggcatcac ggtgctgacc aggggtgaca 1320
255 gcacttcag tactaggagt accgggaagc tgtccaaagc aggttccgag tcttcagca 1380
256 gtgcaggctc ctcaggatcg ctgtcccgca cccatccacc tctccagagc acaccctag 1440

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257 tctcaggtgt ggcagctggc tctccaggct gtgtgcctta tccagagaat ggaatagggg 1500
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259 tcccgcctgg aagcatcctt cttaatccac acacaggcca gccctttgtg aatcccgatg 1620
260 gaactcctgc aatatacaac ccacccacca gtcagcagcc cctgcgaagc gccatggtgg 1680
261 ggcagtccca acagcagccg ccacagcagc agccctcccc gcagcccaa cagcaggtcc 1740
262 agccaccgca gccacagatg gcaggccctc tggctactca gtctgtccag gggctgcagg 1800
263 cttcctccca gtcagtgcaa tatccggcag tctcttttcc tcccagcac ctctacctg 1860
264 tgtctccaac gcagcacttt cccatgagag atgatgtggc aacacagttt ggccagatga 1920
265 ccctgagccg gcagtcctcg ggggagactc ctgaaccccc atcaggtcct gtctacccat 1980
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267 agcttcctac aggaggattc tcaggctctg gccctcccat ctcccagcag gtccctccagc 2100
268 cccctccctc accacaggga ttctgtcaac agcctccgcc tgcacagatg cctgtatat 2160
269 attacccatc tggtcagtac cctacctcaa ccacgcaaca gtaccggccc atggccccgg 2220
270 ttcagtacaa cgctcagagg agtcaacaga tgccacaggc agcacagcaa gcaggttacc 2280
271 agccagtctt gtctgggtcaa cagggtattc aaggccta atagggtgcag cagccacctc 2340
272 agagtcagaa cgtgataaat aaccaacaag gaactccggt gcaaagcgtg atgggttcct 2400
273 acccaacaat gtcttcttat cagggtgcaa tgacccaggg ttctcaagga ctgccccagc 2460
274 agtcatacca acagccaatc atgctaccta accaggcagg tcaagggtca ctcccagcca 2520
275 ctggaatgcc tgtttactgt aatgtcacac cgcccacccc tcagaacaac cttaggctga 2580
276 ttggcccaca ctgcccctcc agcactgtcc cagtgtgtc agctagctgc agaacaaact 2640
277 gtgcaagtat gagcaatgct gggtggcagg tcaaatctc agagctctgg ctgtggtaca 2700
278 tttcttcaga tatttctcat ggctttgat ggaagaggaa caagggtgga aaactggctg 2760
279 aggacttaag tattcactca aactcaa atgtgtgtc ggtattctgt aaaaagtaaa 2820
280 caaagactaa tatacacgtt agctggttaa tgggtgcata ttctgtcatg tctgctaggt 2880
281 atgcctttat agcttagcta gtgacatgaa ttcataagg taagattctc tctaccact 2940
282 gaataccact gtgtagatta taatatccct aatttggatt agttttgtac tttgtgttga 3000
283 gtttgtgatg ctaaaagtat ttaaaaatta tatactaaat cacattgtac caaagctgta 3060
284 atggaaaagc aaagaagaac tgatgaattg aaggaataat ttatatacat tatagagttt 3120
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300 tgtttactg 69
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304 <211> LENGTH: 23
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
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309 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA Primer
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315 <210> SEQ ID NO: 6

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date